09/682,769

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DB=USPT,JPAB,EPAB,DWPI; PLUR=YES; OP=ADJ			
L18	l13 and glyphosate	11	L18
L17	l13 and (acala riata RR or DP 409 B/RR)	0	L17
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L15	l13 and PV-GHGT07(1445)	1	L15
L14	L13 and roundup ready	0	L14
L13	L12 and (hybridiz$4 near5 probe$1)	50	L13
L12	(cotton$1 or gossypium hirsutum) near5 (DNA or nucleic acid or polynucleotide$1)	150	L12
L11	cotton$1 or gossypium hirsutum	118888	L11
L10	L9 and hybridiz$4	1	L10
L9	l7 and (DNA or nucleic acid$1)	4	L9
L8	L7 and DNA	4	L8
L7	L6 and cotton$1	7	L7
L6	roundup ready	110	L6
L5	rounddup ready	0	L5
L4	roundup ready near20 cottton$1	0	L4
L3	roundup ready near5 cotton$1 near5 DNA	0	L3
L2	roundup ready	110	L2
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END OF SEARCH HISTORY

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L18: Entry 4 of 11 File: USPT Oct 30, 2001

DOCUMENT-IDENTIFIER: US 6308458 B1
TITLE: Herbicide-tolerant plants and methods of controlling the growth of undesired vegetation

Brief Summary Text (12):
Unfortunately, herbicides that exhibit greater potency, broader weed spectrum and more rapid degradation in soil can also have greater crop phytotoxicity. One solution applied to this problem has been to develop crops that are resistant or tolerant to herbicides. Crop hybrids or varieties resistant to the herbicides allow for the use of the herbicides without attendant risk of damage to the crop. Development of resistance can allow application of a herbicide to a crop where its use was previously precluded or limited (e.g. to pre-emergence use) due to sensitivity of the crop to the herbicide. For example, U.S. Pat. No. 4,761,373, incorporated herein by reference, is directed to plants resistant to various imidazolinone or sulfonamide herbicides. The resistance is conferred by an altered acetohydroxyacid synthase (AHAS) enzyme. U.S. Pat. No. 4,975,374, incorporated herein by reference, relates to plant cells and plants containing a gene encoding a mutant glutamine synthetase (GS) resistant to inhibition by herbicides that were known to inhibit GS, e.g. phosphinothricin and methionine sulfoximine. U.S. Pat. No. 5,013,659, incorporated herein by reference, is directed to plants that express a mutant acetolactate synthase (ALS) that renders the plants resistant to inhibition by sulfonylurea herbicides. U.S. Pat. No. 5,162,602, incorporated herein by reference, discloses plants tolerant to inhibition by cyclohexanedione and aryloxyphenoxypropanoic acid herbicides. The tolerance is conferred by an altered acetyl coenzyme A carboxylase(ACCase). U.S. Pat. No. 5,554,798, incorporated herein by reference, discloses transgenic glyphosate resistant maize plants, which tolerance is conferred by an altered 5-enolpyruvyl-3-phosphoshikimate (EPSP) synthase gene.

Brief Summary Text (21):
The present invention provides DNA molecules isolated from wheat, soybean, cotton, sugar beet, oilseed rape, rice, sorghum, and sugar cane encoding enzymes having protoporphyrinogen oxidase (protox) activity and chimeric genes comprising such DNA. Sequences of such DNA molecules are set forth in SEQ ID NOs:9 (wheat), 11 (soybean), 15 (cotton), 17 (sugar beet), 19 (oilseed rape), 21 (rice), 23 (sorghum), and 36 (sugar cane).

Brief Summary Text (47):
SEQ ID NO:15: DNA coding sequence for a cotton protox-1 protein.

Brief Summary Text (131):
In still another aspect, the present invention is directed to an isolated DNA molecule that encodes a cotton protox enzyme and that comprises a nucleotide sequence that hybridizes to the coding sequence shown in SEQ ID NO:15 under the following hybridization and wash conditions:

Brief Summary Text (149):
The isolated eukaryotic protox sequences taught by the present invention may be manipulated according to standard genetic engineering techniques to suit any desired purpose. For example, the entire protox sequence or portions thereof may be used as probes capable of specifically hybridizing to protox coding sequences and messenger RNA's. To achieve specific hybridization under a variety of conditions, such probes include sequences that are unique among protox coding sequences and are preferably at least 10 nucleotides in length, and most preferably at least 20 nucleotides in length. Such probes may be used to amplify and analyze protox coding sequences from a chosen organism via the well known process of polymerase chain reaction (PCR). This technique may be useful to isolate additional protox coding sequences from a desired organism or

as a diagnostic assay to determine the presence of protox coding sequences in an organism.

Brief Summary Text (152):
The invention further embodies the use of a nucleotide probe capable of specifically hybridizing to a plant protox gene or mRNA of at least 10 nucleotides length in a polymerase chain reaction (PCR).

Brief Summary Text (153):
In a further embodiment, the present invention provides probes capable of specifically hybridizing to a eukaryotic DNA sequence encoding a protoporphyrinogen oxidase activity or to the respective mRNA and methods for detecting the DNA sequences in eukaryotic organisms using the probes according to the invention.

Brief Summary Text (157):
(a) preparing a nucleotide probe capable of specifically hybridizing to a plant protox gene or mRNA, wherein the probe comprises a contiguous portion of the coding sequence for a protox protein from a plant of at least 10 nucleotides length;

Brief Summary Text (161):
(a) preparing a nucleotide probe capable of specifically hybridizing to a plant protox gene or mRNA, wherein the probe comprises a contiguous portion of the coding sequence for a protox protein from a plant of at least 10 nucleotides length;

Brief Summary Text (166):
(b) hybridizing the library with a probe molecule; and

Brief Summary Text (371):
Particularly preferred is a chimeric gene, wherein the DNA molecule encodes a protein from cotton having protox-1 activity, preferably wherein the protein comprises the amino acid sequence set forth in SEQ ID NO:16.

Brief Summary Text (415):
Useful markers include peptides providing herbicide, antibiotic or drug resistance, such as, for example, resistance to hygromycin, kanamycin, G418, gentamycin, lincomycin, methotrexate, glyphosate, phosphinothricin, or the like. These markers can be used to select cells transformed with the chimeric DNA constructs of the invention from untransformed cells. Other useful markers are peptidic enzymes that can be easily detected by a visible reaction, for example a color reaction, for example luciferase, .beta.-glucuronidase, or .beta.-galactosidase.

Brief Summary Text (463):
In another preferred embodiment, the transit peptide of a DNA molecule encoding a 5-enolpyruvyl-3-phosphoshikimate synthase (EPSP synthase) is mutated or removed. The resulting DNA molecule is fused to a promoter capable of expression in plant plastids and homoplasmic plants harboring such constructs in their plastid genomes are obtained. These plants are resistant to herbicidal compounds that naturally inhibit EPSP synthase, in particular glyphosate. In another preferred embodiment, the transit peptide of a DNA molecule encoding a acetolactate synthase (ALS) is mutated or removed. The resulting DNA molecule is fused to a promoter capable of expression in plant plastids and homoplasmic plants harboring such constructs in their plastid genome are obtained. These plants are resistant to herbicidal compounds that naturally inhibit ALS, in particular sulfonylureas. In another preferred embodiment, the transit peptide of a DNA molecule encoding a acetoxyhydroxy acid synthase (AHAS) is mutated or removed. The resulting DNA molecule is fused to a promoter capable of expression in plant plastids and homoplasmic plants harboring such constructs in their plastid genome are obtained. These plants are resistant to herbicidal compounds that naturally inhibit AHAS, in particular, imidazolinone and sulfonamide herbicides. In another preferred embodiment, the transit peptide of a DNA molecule encoding an acetylcoenzyme A carboxylase (ACCase) is mutated or removed. The resulting DNA molecule is fused to a promoter capable of expression in plant plastids and homoplasmic plants harboring such constructs in their plastid genome are obtained. These plants are resistant to herbicidal compounds that naturally inhibit ACCase, in particular cyclohexanedione and arylphenoxypropanoic acid herbicides. In another preferred embodiment, the transit peptide of a DNA molecule encoding a glutamine synthase (GS) is mutated or removed.

The resulting DNA molecule is fused to a promoter capable of expression in plant plastids and homoplasmic plants harboring such constructs in their plastid genome are obtained. These plants are resistant to herbicidal compounds that naturally inhibit GS, in particular phosphinothricin and methionine sulfoximine.

Other Reference Publication (25):
Datta et al., "Transformation of the Tobacco Chloroplast Genome with the aroA Gene to Confer Glyphosate Tolerance," Supplement to Plant Physiology, 111(2): 790 (1996).

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L18: Entry 1 of 11 File: USPT May 13, 2003

DOCUMENT-IDENTIFIER: US 6563022 B2
TITLE: Cotton plants with improved cotton fiber characteristics and method for producing cotton fibers from these cotton plants

Brief Summary Text (11):
In recent years, gene recombinant technique has made remarkable progress, and several reports have been made on the successful variety improvement in certain kinds of plants (e.g., cotton, soybean, corn, tomato) by introduction and expression of a particular gene in these plants to confer a desired genetic trait thereon. There have been developed and put to practical use, for example, cotton plants with improved insect resistance by introduction of a gene coding for BT toxin (i.e., insecticidal protein toxin produced by Bacillus thuringiensis) or cotton plants with improved herbicide (Glyphosate) resistance by introduction of a gene coding for 5-enol-pyruvil-shikimic acid 3-phosphate synthetase.

Detailed Description Text (17):
The phage plaque pattern of the cDNA library prepared by the above method in section 1(1) is replicated onto two filters, which are hybridized with each of the .sup.32 P-labelled cDNA probes prepared by the same method as described in section 1(1) from the ovules on the 5th day after the flowering and from the ovules on the 25th day after the flowering. The cDNA corresponding to the desired gene can be selected by detection of a positive hybridization signal only from the cDNA probe prepared from the ovules on the 5th day after the flowering.

Detailed Description Text (26):
The phage plaque pattern of the cDNA library prepared by the above method in section 2(1) is replicated onto a filter, which is hybridized with a .sup.32 P-labelled cDNA probe corresponding to the cotton catalase gene (Ni W., Turley R. B., Trelease R. N., Biochem. Biophys. Acta., 1049, 219-222 (1990)). The cDNA corresponding to the desired gene can be selected by detection of a positive hybridization signal.

Detailed Description Text (35):
The colony pattern of the cDNA library prepared by the above method in section 3(1) is replicated onto a filter, which is hybridized with a .sup.32 P-labelled cDNA probe that can be synthesized by a commercially available DNA synthesizer from the amino acid sequence of horseradish peroxidase (Welinder, K. G., FEBS Lett., 72, 19-23 (1976)). The cDNA corresponding to the desired gene can be selected by detection of a positive hybridization signal.

Detailed Description Text (72):
As a result, 34 positive clones hybridized with the probe for the fiber elongation stage rather than for the fiber non-elongation stage were selected. The particularly strongly hybridized clone was designated KC22 and further analyzed.

CLAIMS:

1. A cotton plant of the genus Gossypium with improved cotton fiber characteristics, comprising an expression cassette containing a polynucleotide coding for catalase operably linked to a promoter that directs expression in cotton fiber cells, so that the polynucleotide is expressed in cotton fiber cells to improve fiber length, fiber fineness, or fiber strength as compared to cotton fiber cells from a non-transformed cotton plant.

2. The cotton plant according to claim 1, wherein the catalase polynucleotide is derived from a plant.

3. The cotton plant according to claim 2, the catalase polynucleotide is derived from a pea plant.

4. The cotton plant according to claim 1, wherein the catalase polynucleotide has a nucleotide sequence extending from bps 57 to 1541 of SEQ ID NO: 2.

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Search Results - Record(s) 21 through 30 of 50 returned.

☐ 21. 6183958 . 06 May 98; 06 Feb 01. Probes for variance detection. Stanton, Jr.; Vincent P.. 435/6; 435/69.1 536/23.1 536/24.3. C07H021/04 C12Q001/68 C12N015/00.

☐ 22. 6166301 . 30 Jun 98; 26 Dec 00. Method for assaying genetic attributes in cotton fiber cells. Delmer; Deborah P., et al. 800/314; 435/427 435/469 536/23.6 536/24.1 800/278 800/287 800/294. C12N015/82 C12N015/84 C12N005/04 C12N015/29 A01H004/00.

☐ 23. 6114115 . 28 Apr 95; 05 Sep 00. Use of immobilized mismatch binding protein for detection of mutations and polymorphisms, and allele identification. Wagner, Jr.; Robert E.. 435/6; 435/91.2. C12Q001/68 C12P019/34.

☐ 24. 6096950 . 18 Nov 96; 01 Aug 00. Cotton fiber-specific promoters. John; Maliyakal E.. 800/314; 435/320.1 536/24.1. A01H005/00 C07H021/04 C12N015/82.

☐ 25. 6084155 . 22 Jun 98; 04 Jul 00. Herbicide-tolerant protoporphyrinogen oxidase ("protox") genes. Volrath; Sandra L., et al. 800/300; 435/320.1 435/419 435/440 536/23.2 536/23.6 800/306 800/312 800/314 800/317.3 800/320 800/320.1 800/320.2 800/320.3. A01H005/00 A01H005/10 C12N005/14 C12N015/29 C12N015/52 C12N015/82.

☐ 26. 6040504 . 10 Feb 98; 21 Mar 00. Cotton promoter. Rice; Douglas, et al. 800/314; 435/252.3 435/320.1 435/419 536/23.1 536/24.1 800/298. A01H005/00 C07H021/04 C12N001/21 C12N005/14 C12N015/82.

☐ 27. 6027877 . 04 Nov 93; 22 Feb 00. Use of immobilized mismatch binding protein for detection of mutations and polymorphisms, purification of amplified DNA samples and allele identification. Wagner, Jr.; Robert E.. 435/6; 435/7.5 436/518 436/528 436/529 436/530 436/531. C12Q001/68 G01N033/543.

☐ 28. 6023012 . 30 Mar 98; 08 Feb 00. DNA molecules encoding plant protoporphyrinogen oxidase. Volrath; Sandra L., et al. 800/300;. C12N015/29 C12N015/51 C12N015/82.

☐ 29. 6018105 . 28 Feb 97; 25 Jan 00. Promoters from plant protoporphyrinogen oxidase genes. Johnson; Marie A., et al. 800/298; 435/320.1 435/419 536/24.1. A01H005/00 C07H021/04 C12N005/14 C12N015/82.

☐ 30. 5981834 . 27 Jan 97; 09 Nov 99. Genetically engineering cotton plants for altered fiber. John; Maliyakal E., et al. 800/278; 435/419 530/350 536/23.6 800/287 800/290. A01H004/00 C07H021/04 C07K014/415 C12N005/14.

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L13: Entry 30 of 50 File: USPT Nov 9, 1999

DOCUMENT-IDENTIFIER: US 5981834 A
TITLE: Genetically engineering cotton plants for altered fiber

Detailed Description Text (6):
The invention envisions the genetic transformation of one variety of cotton plant by the introduction of DNA constructions including a fiber gene from a second, different variety of cotton plant or by the alteration of a native fiber gene. Non-limiting examples which may be used for the present invention as either the source of the fiber genes or the plant which is transformed include plants belonging to (Gossypium arboreum. G. herbaceum, G. barbadense), and (G. hirsutum). Additionally, the process of the present invention may incorporate fiber genes from other exotic plants which produce cellulose fiber. Many of these plants will have fibers with one or more desirable qualities, which can then be incorporated into the cotton plant. Such plants include the Silk Cotton Tree (Kapok, Ceiba pentandra), Desert Willow, Creosote Bush, Winterfat, Balsa, Ramie, Kenaf, Hemp, Roselle, Jute, Sisal Abaca and Flax.

Detailed Description Text (9):
The identification of fiber genes preferably begins with the identification of fiber specific mRNA's. The sequences of several cDNA clones from such fiber specific mRNA are given below. These cDNA clones were all created by analysis of cotton fiber mRNAs. Conventional method of isolating RNA's from plant cells do not work well with cotton fiber cells. The isolation of high purity DNA or RNA from cotton cells has been notoriously difficult, partly due to the phenolic terperiods and tannins present in cotton cells. Katterman et al., Preparative Biochemistry, 13, pp. 347-359 (1983) It has been found that certain modifications of RNA isolation techniques permit the isolation of RNA from cotton fiber cells. The protocol used was based on that set forth in Chirqwin et al., Biochemistry, 18, pp. 5294-5299 (1979), modified to include higher buffering capacity, alkaline pH, and the addition of polyvinyl pyrrolidone (PVP). The PVP, in particular, is believed to form hydrogen bonding to phenolics, and are then removed in subsequent steps. While others have suggested the use of PVP for other plant systems, the significance of the addition of this additive to the successful isolation of total mRNA from cotton fiber cells has not previously been demonstrated. Lichtenstein and Draper in "Genetic Engineering of Plants, DNA Cloning, Vol II, Glover, Ed., pp. 101-110 (1985).

Detailed Description Text (30):
Genomic DNA from Sea Island cotton and from Kapok were prepared according to the methods of Richards, E. described in Current Protocols in Molecular Biology, (Eds. Ausbel, F. M. et al.) Wiley, (1987) pp. 2.3.1 2.3.3, with the following modification: the frozen plant material was homogenized in extraction buffer containing 1% polyvinyl pyrrolidone. The purified genomic DNA was digested with restriction endonucleases and transferred to nitro-cellulose filters by the Southern blotting technique. Southern, E. M., J. Mol. Biol., 98: 503-517 (1975).

Detailed Description Text (76):
Similarly, hybridizations of the first five cDNA clones have been conducted with genomic DNA from a number of cotton species, including herbaceum, arboreum, anomalum, sturtianum, australe, nelsonii, thurberi, davidsonii, stocksii, somelense, longicalyx, and bickii. Many of these species are not grown commercially but grow wild in various locales. The DNA from all these cotton species showed hybridization with these five cDNA clones, indicating that these genes are conserved to a certain degree among cotton species. However, while all showed hybridization, there was variation in the size of the DNA fragments from the genomic DNA to which the cDNA clones hybridized suggesting structural differences among the corresponding genes in the various species. Similar results were found for at least one cDNA clone (E6) with genomic Kapok DNA. This supports the notion that these same cDNA clones can be used to

identify and isolate corresponding fiber genes from a wide variety of fiber producing plants.

Detailed Description Text (89):
Once the DNA has been purified from the phage genomic clones (Ausubel et al., PP. 1.10.1 to 1.13.6) the insert DNAs (10 to 15 Kbs) may be characterized in terms of their restriction maps (supra, PP. 3.1.1 to 3.3.2). The different restriction fragments may be separated on agarose gels and Southern blotted. The blots may then be hybridized to cDNA probes. This procedure will enable one to identify smaller fragments (about 5 to 10 Kb) that contains the homologous cDNA sequence. This fragment may then be subcloned (supra, 3.16.1 to 3.16.11) into plasmid vectors such as pGEM5zf (Promega, Madison) or Bluescript SK, KS (Stratagene, Calif.). All further manipulations such as promoter identifications, transcription maps and gene size determinations may then be done using the subclones.

Detailed Description Text (90):
Mapping the gene transcripts by nuclease protection may also be done. Single stranded DNA probes may be generated from the Bluescript subclones and hybridized to poly(A).sup.+ RNA from fiber cells. The hybridized portions that are protected from nuclease action will be determined as described by Calzone F. J. et al. in Methods in Enzymology, Vol. 152 (Eds. Berger, S. L. and Kimmel, A. R.) pp. 611 to 629. Furthermore, mapping the 5' termini by cDNA primer extension is also described (supra pp. 629 to 632). These strategies will determine the size of the gene, as well as precise boundaries of the gene transcript, or coding region for the fiber gene, in the subclone. That portion of the DNA may then be sequenced if desired.

Detailed Description Text (145):
Antisense E6 Genes (AS-52 and AS-58). The 5'-end of coding region of the E6 gene (described above) contains an Nco site where translation initiation occurs. At the 3'-end of the gene there is a Hind III site. These two sites were used to clone a modified E6 gene so that an antisense RNA is produced on transcription. This was accomplished by deleting the Nco site from the 5'-end coding region and inserting a Hind III site in its place. The 3'-end was similarly modified by inserting an Nco site. The coding region of E6 gene was amplified by PCR using two primers and cotton genomic DNA clone SKSIE6-2AH3. (Saiki et al., Science, 239; 487-491, 1988). The two PCR primers we used were: 5'-ATG CGC AAG CTT TGG CTT CCT CAC CAA AAC-3' (called MEJ4, SEQ ID NO: 19) and 5'-GTC GAC CAT GGG TTC GAA CTC TTC CTC-3' (called MEJ-5, SEQ ID NO: 20).

Detailed Description Text (170):
Fiber properties were measured by either Star Lab (2121 Dutch Valley, Knoxville, Tenn.) or by Cotton Incorporated (Raleigh, N.C.). Table 2, below, shows transgenic cotton plants containing various cDNA and genomic DNA constructs. Transgenic plants and fibers from each of these groups were analyzed. The fiber measurements for each group are presented in the following sections.

Other Reference Publication (18):
Zhou, G.Y., et al., "Introduction of Exogenous DNA into Cotton Embryos," Methods in Enzymology, 101:433-481 (1983).

CLAIMS:

1. A cotton plant comprising in its genome a foreign DNA sequence which has been introduced other than by Mendelian inheritance into the plant or its parents, in which the foreign DNA sequence expresses a foreign protein, wherein said sequence is selected from the group consisting of CDFB15A1E6, CDFB15A1H6, CDFB15A1C12, CDFB15A1-B8, and CKFB10-A11 and in which the foreign protein coding sequence is expressed in fiber cells of the plant to produce a protein not natively present in the cotton plant.

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Search Results - Record(s) 1 through 10 of 50 returned.

☑ 1. 6566588 . 09 Jun 99; 20 May 03. Plants transformed with a nucleic acid encoding the hypersensitive response associated protein amphipathetic protein-1. Feng; Teng-Yung, et al. 800/301; 536/23.6. C12N015/29 C12N015/82.

☐ 2. 6563022 . 16 Apr 01; 13 May 03. Cotton plants with improved cotton fiber characteristics and method for producing cotton fibers from these cotton plants. Kasukabe; Yoshihisa, et al. 800/290; 435/192 435/419 435/468 800/278 800/298 800/314. A01H001/00 A01H005/00 C12N009/08 C12N005/04 C12N015/82.

☐ 3. 6559363 . 16 Apr 01; 06 May 03. Cotton plants with improved cotton fiber characteristics and method for producing cotton fibers from these cotton plants. Allen; Randy Dale, et al. 800/314; 435/468 536/23.6 800/278 800/290. A01H005/00 A01H001/00 C07H021/04 C12N015/82.

☐ 4. 6544730 . 27 Oct 97; 08 Apr 03. High density polymorphic genetic locus. Deininger; Prescott, et al. 435/6; 435/91.1 435/91.2 536/23.1 536/24.3 536/24.31 536/24.33. C12Q001/68 C12P019/34 C07H021/02.

☐ 5. 6541448 . 11 May 01; 01 Apr 03. Polypeptide compositions toxic to anthonomus insects, and methods of use. Isaac; Barbara, et al. 514/2; 424/246.1 530/350. C07K014/00.

☐ 6. 6541238 . 10 Oct 95; 01 Apr 03. Recombinant cellulose synthase. Saxena; Inder Mohan, et al. 435/252.3; 435/193 435/194 435/252.33 435/257.2 435/320.1 435/325 435/419. C12N001/20 C12N009/10 C12N009/12 C12N015/00.

☐ 7. 6514760 . 07 Jul 00; 04 Feb 03. Jointless gene of tomato. Mao; Long, et al. 435/419; 435/320.1 536/23.6. C12N015/29 C12N015/82 C07H021/04.

☐ 8. 6468523 . 02 Nov 98; 22 Oct 02. Polypeptide compositions toxic to diabrotic insects, and methods of use. Mettus; Anne-Marie Light, et al. 424/93.2; 424/93.461 514/12 514/2 530/350 530/825. A01N063/00 A01N037/18 C07K014/325.

☐ 9. 6432628 . 25 Aug 98; 13 Aug 02. Caspase-14, an apoptotic protease, nucleic acids encoding and methods of use. Alnemri; Emad S., et al. 435/4; 435/7.1 435/7.4 435/7.71 435/7.72. C12Q001/00 G01N033/53 G01N033/573.

☐ 10. 6406847 . 17 Mar 99; 18 Jun 02. Mismatch repair detection. Cox; David R., et al. 435/6; 435/91.2 536/23.1 536/24.3 536/24.31 536/24.33. C12Q001/68 C12P019/31 C07H021/07 C07H021/04.

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L13: Entry 1 of 50 File: USPT May 20, 2003

DOCUMENT-IDENTIFIER: US 6566588 B1
TITLE: Plants transformed with a nucleic acid encoding the hypersensitive response associated protein amphipathetic protein-1

Detailed Description Text (32):
To test for the distribution of ap-1 in various plants, genomic DNA was isolated from pepper, tomato, tobacco, cotton, Arabidopsis thaliana and Petunia sp. according to Nelson, Id. For PCR detection of ap-1 sequences, a 5' primer in the ap-1 coding sequence (5'-AATAGAATTTGATTGCCCAGA-3'; SEQ ID NO:9) and 3' primer (5'-CATCTTGGTCAAAGTTTGAATC-3'; SEQ ID NO:8) in the 3' untranslated region were used. The 5' primer and the 3' primer was expected to produce a 373 bp PCR product. The PCR was performed in MgCl.sub.2 buffer containing 1 mM dNTP, 2.5 units of Taq DNA polymerase, 200 ng genomic DNA and 5% dimethylsulfoxide. The amplification parameters were as follows: 5 minutes at 94.degree. C.; 5 cycles of 1 minute at 94.degree. C., 1 minute at 51.degree. C., and 1 minute at 72.degree. C.; and 30 cycles of 45 seconds at 94.degree. C., 1 minute at 51.degree. C., and 1 minute at 72.degree. C.; and 5 minutes at 72.degree. C.

Detailed Description Text (33):
A 373 bp fragment could be amplified from pepper, tomato, tobacco, Petunia, and cotton genomic DNA but not from Arabidopsis genomic DNA.

Detailed Description Text (36):
In order to transiently express pepper AP-1 in vivo, the pap1 coding region was subcloned into a bamboo mosaic potexvirus satellite (satBaMV) vector, which is described in Lin et al., Proc Natl Acad Sci USA 93:3138 (1996), hereby designated BSAP1. BASP1 was used to in vitro transcribe an RNA containing the 432 bp ap-1 open reading frame and about 400 bp of viral sequence. The BaMV-L and satBaMV vector transcripts were inoculated, along with the ap-1 transcript, into the tobacco Nicotiana benthamiana. Northern blot hybridization was used to detect the replication of viral RNA in tobacco. The total RNA extracted 7 days after inoculation was separated on 1% agarose gels, transferred to nylon membranes, and hybridized with a probe specific to the 3' end of satBaMV (+)RNA as described in Lin et al., (1996) Id. The Northern indicated that the BSAP1 RNA was expressed in the tobacco.

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L1 1 PV-GHGT07

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DN 136:351437
TI Genomic/transgene insert sequences in cotton event **PV-GHGT07**(1445) and primers for detection thereof
IN Rangwala, Tasneem S.; Ye, Minwei
PA Monsanto Technology LLC, USA
SO PCT Int. Appl., 30 pp.
CODEN: PIXXD2
DT Patent
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	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2002034946	A2	20020502	WO 2001-US32258	20011017
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	AU 2002015363	A5	20020506	AU 2002-15363	20011017
	US 2002120964	A1	20020829	US 2001-682769	20011017
PRAI	US 2000-243190P	P	20001025		
	WO 2001-US32258	W	20011017		

AB The present invention provides DNA compns. and assays for detecting the presence of the DNA compns. in **PV-GHGT07**(1445) cotton event based on the DNA sequence of the recombinant construct inserted into the cotton genome and of the genomic sequences flanking the insertion

site. Kits and conditions useful in conducting the assays are provided which can be used for detection of zygosity of transgenic cotton resistant to glyphosate.

TI Genomic/transgene insert sequences in cotton event **PV-GHGT07**(1445) and primers for detection thereof

AB The present invention provides DNA compns. and assays for detecting the presence of the DNA compns. in **PV-GHGT07**(1445) cotton event based on the DNA sequence of the recombinant construct inserted into the cotton genome and of the genomic sequences flanking the insertion site. Kits and conditions useful in conducting the assays are provided which can be used for detection of zygosity of transgenic cotton resistant to glyphosate.

IT Cotton
(event **PV-GHGT07**(1445), glyphosate tolerance in; genomic/transgene insert sequences in cotton event **PV-GHGT07**(1445) and primers for detection thereof)

IT Primers (nucleic acid)
RL: AGR (Agricultural use); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(for detection of insertion in transgenic cotton; genomic/transgene insert sequences in cotton event **PV-GHGT07**(1445) and primers for detection thereof)

IT Test kits
(for detection of transgenic cotton; genomic/transgene insert sequences in cotton event **PV-GHGT07**(1445) and primers for detection thereof)

IT Amplicon
RL: AGR (Agricultural use); BSU (Biological study, unclassified); BIOL (Biological study); USES (Uses)
(for detection of transgenic cotton; genomic/transgene insert sequences in cotton event **PV-GHGT07**(1445) and primers for detection thereof)

IT Breeding, plant
(for glyphosate resistance; genomic/transgene insert sequences in cotton event **PV-GHGT07**(1445) and primers for detection thereof)

IT Genotypes
(heterozygosity, detection of; genomic/transgene insert sequences in cotton event **PV-GHGT07**(1445) and primers for detection thereof)

IT Gene
RL: AGR (Agricultural use); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(insertion, for glyphosate tolerance in cotton; genomic/transgene insert sequences in cotton event **PV-GHGT07**(1445) and primers for detection thereof)

IT DNA sequences
(of genomic/transgene insertion; genomic/transgene insert sequences in cotton event **PV-GHGT07**(1445) and primers for detection thereof)

IT Herbicides
(resistance of, in transgenic plants; genomic/transgene insert sequences in cotton event **PV-GHGT07**(1445) and primers for detection thereof)

IT 420277-48-1 420277-49-2 420277-50-5 420277-51-6 420277-52-7 420277-53-8
RL: AGR (Agricultural use); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(nucleotide sequence of primer; genomic/transgene insert sequences in cotton event **PV-GHGT07**(1445) and primers for detection thereof)

IT 420277-54-9 420277-55-0
RL: AGR (Agricultural use); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)

(nucleotide sequence; genomic/transgene insert sequences in cotton event **PV-GHGT07**(1445) and primers for detection thereof)

IT 1071-83-6, Glyphosate
RL: AGR (Agricultural use); BSU (Biological study, unclassified); BIOL (Biological study); USES (Uses)
(resistance of, in cotton; genomic/transgene insert sequences in cotton event **PV-GHGT07**(1445) and primers for detection thereof)

IT 420281-20-5 420281-21-6 420281-22-7, 7: PN: WO0234946 SEQID: 7 unclaimed DNA 420281-23-8, 8: PN: WO0234946 SEQID: 8 unclaimed DNA
RL: PRP (Properties)
(unclaimed nucleotide sequence; genomic/transgene insert sequences in cotton event **PV-GHGT07**(1445) and primers for detection thereof)

L3 ANSWER 1 OF 2 CAPLUS COPYRIGHT 2003 ACS
AN 1990:418772 CAPLUS
DN 113:18772
TI Molecular characteristics of the chalcone synthetase gene family of tetraploid cotton Gossypium hirsutum 108 F
AU Byzova, M. V.; Kraev, A. S.; Skryabin, K. G.
CS Inst. Mol. Biol., Moscow, USSR
SO Doklady Akademii Nauk SSSR (1990), 311(3), 742-4, 1 plate [Genet.]
CODEN: DANKAS; ISSN: 0002-3264
DT Journal
LA Russian
AB Tetraploid **cotton** variety 108F genomic **DNA** restriction fragments in Escherichia coli were blot **hybridized** with DNA complementary to Antirrhinum majus chalcone synthetase gene exon 1 and 2 (**probe** 1) or exon 3 (**probe** 2). **Probe** 2 identified 3-4 hybridizing DNA fragments, whereas, **probe** 1 identified .apprx.9 hybridizing regions of different intensities suggesting the presence of at least 3 regions in the cotton genome coding for chalcone synthetase. With the use of clone CGH3, which hybridized to **probe** 2, homol. RNA transcripts of 1200 bp were identified in cotton cotyledon, etiolated hypocotyl, and root tissue. Clone CGH3 contained part of the protein coding region and the 3' nontranscribed region.
AB Tetraploid **cotton** variety 108F genomic **DNA** restriction fragments in Escherichia coli were blot **hybridized** with DNA complementary to Antirrhinum majus chalcone synthetase gene exon 1 and 2 (**probe** 1) or exon 3 (**probe** 2). **Probe** 2 identified 3-4 hybridizing DNA fragments, whereas, **probe** 1 identified .apprx.9 hybridizing regions of different intensities suggesting the presence of at least 3 regions in the cotton genome coding for chalcone synthetase. With the use of clone CGH3, which hybridized to **probe** 2, homol. RNA transcripts of 1200 bp were identified in cotton cotyledon, etiolated hypocotyl, and root tissue. Clone CGH3 contained part of the protein coding region and the 3' nontranscribed region.

L3 ANSWER 2 OF 2 CAPLUS COPYRIGHT 2003 ACS
AN 1985:465976 CAPLUS
DN 103:65976
TI Cloning of cotton repetitive sequences
AU Shen, Weifang; Zhou, Guangyu
CS Shanghai Inst. Biochem., Acad. Sin., Shanghai, Peop. Rep. China
SO Shengwu Huaxue Yu Shengwu Wuli Xuebao (1985), 17(1), 146-54
CODEN: SHWPAU; ISSN: 0582-9879
DT Journal
LA Chinese
AB To study the structure and function of plant repetitive sequences, cotton repetitive sequences were cloned by using phage M13mp7 as a vector. Sea Island cotton 416 DNA was sheared to .apprx.2-4 kilobases, denatured, renatured to C0t 20, treated with S1 nuclease, RI sticky ends added, recombined with M13mp7/RI and cloned. The length of the cloned repetitive DNA fragments was estd. by gel electrophoresis. Their distribution is .apprx. 50 base pairs-1.5 kilobases. All cloned **DNA** can **hybridize** with nick-translated Sea Island **cotton** 416 **DNA**, but the extent of hybridization varies. Using labeled clone No. 23 as a Southern blot **probe** with different genomic DNA of Sea Island cotton and Upland cotton it was shown that a widely spread repetitive sequence was cloned in No. 23. It is a sequence common to Sea Island Cotton and Upland cotton. The DNA sequence of No. 23 was detd. It is probably a highly repetitive sequence.
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